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Om protein - protein search, using sw model

Run on: September 24, 2003, 15:43:18 ; Search time 63.5263 Seconds
(without alignments)
2848.398 Million cell updates/sec

Title: US-09-974-973a-19

Perfect score: 5788

Sequence: 1 MSTHTSSTLPAFKKKILVANR. RVVWPAATKVEGGDLIVVS 1140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: _Geneseq_19Jun03:*

2: /SIBSL/gcdata/geneseq/geneseqp-emb1/AA1980.DAT:*

3: /SIBSL/gcdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIBSL/gcdata/geneseq/geneseqp-emb1/AA1983.DAT:*

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22: /SIBSL/gcdata/geneseq/geneseqp-emb1/AA2001.DAT:*

23: /SIBSL/gcdata/geneseq/geneseqp-emb1/AA2002.DAT:*

24: /SIBSL/gcdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	5788	100.0	1140	22	AMG90511	C glutamicum prote
2	5788	100.0	1140	22	AAB67129	Corynebacterium gl
3	5788	100.0	1140	23	AAE25601	corynebacterium gl
4	5788	100.0	1140	23	AAU98053	Corynebacterium wi
5	5784	99.9	1141	21	AAB01436	Pyruvate carboxyl
6	5782	99.9	1140	20	AAW93971	C. glutamicum Pyru
7	5780	99.9	1140	22	AMG93749	C. glutamicum prote
8	5759	99.5	1140	23	AAU98052	Corynebacterium mu
9	5759	99.5	1157	23	AAU98050	Corynebacterium fe

ALIGNMENTS

RESULT 1

ARG90511

ID AAG90511 standard: Protein: 1140 AA.

XX

AC AAG90511;

XX

DT 26-SEP-2001 (first entry)

XX

DE C glutamicic protein fragment. SEQ ID NO: 4265.

XX

KW coryneform bacterium; amino acid synthesis; vitamin; saccharide; organic acid synthesis.

XX

OS corynebacterium glutamicum.

XX

PN EP1108790-A2.

XX

PD 20-JUN-2001.

XX

PF 18-DEC-2000; 2000EP-0127688.

XX

PR 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

XX

PA (KYO) KYOMA HAKKO KOGYO KK.

XX

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX

DR WII; 2001-376931/40.

DR N-PSDB; AAH65730.

XX
 PT Novel polynucleotides derived from Coryneform bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analysing
 PT expression profile or pattern of a gene and identifying homologous gene
 PT
 XX
 PS Claim 17; SEQ ID NO: 4265; 246pp + sequence Listing; English.
 XX
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the coryneform bacterium *Corynebacterium glutamicum*. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of coryneform bacterium, measuring expression amount and
 CC analysing the expression profile or expression pattern of a gene derived
 CC from Coryneform bacterium, and identifying a homologue of a gene derived
 CC from coryneform bacterium. Coryneform bacteria are useful for producing
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described
 CC in the exemplification of the invention.
 Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC European Patent Office.

Sequence 1140 AA;

Query Match 100 %; Score 5788; DB 22; Length 1140;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTHHSISITLPAFKKILVANNGEIAVRAFALETAETVATVYIPREDRGSPFHRSFAEAVR 60
 Db 1 MTHHSISITLPAFKKILVANNGEIAVRAFALETAETVATVYIPREDRGSPFHRSFAEAVR 60
 QY 61 IGTEGSPVKAVALDIDTGAKKVWADATIPGYGFLSENAQLCRCAENITFGPTPEV 120
 Db 61 IGTEGSPVKAVALDIDTGAKKVWADATIPGYGFLSENAQLCRCAENITFGPTPEV 120
 QY 121 LDITDSDKSRAVTAARKAGLIVLAVSTPSNIDEIYKSAQGTYIIFWKAWAGGGGRGMF 180
 Db 121 LDITDSDKSRAVTAARKAGLIVLAVSTPSNIDEIYKSAQGTYIIFWKAWAGGGGRGMF 180
 QY 181 VASPELRLKATEASREAARAFGAGVYERAVINPOHETVQIIGDHTGEVHLYERDCS 240
 Db 181 VASPELRLKATEASREAARAFGAGVYERAVINPOHETVQIIGDHTGEVHLYERDCS 240
 QY 241 LQRHQKVYELPAQHDLDELRDICADEVAKFCRSIGAGTVEFLYDEKGHNFTEN 300
 Db 241 LQRHQKVYELPAQHDLDELRDICADEVAKFCRSIGAGTVEFLYDEKGHNFTEN 300
 QY 301 PRIQEVHTTEEVTDLYKAQMRLAAGATLKEGLTQDKIKHGAACQCRITTEDPQ 360
 Db 301 PRIQEVHTTEEVTDLYKAQMRLAAGATLKEGLTQDKIKHGAACQCRITTEDPQ 360
 QY 361 FRPDGTTAYRSPGGAGGRDLGRDAGLQGEGITAHDMSMVKMCRGSDFEETAVARAQL 420
 Db 361 FRPDGTTAYRSPGGAGGRDLGRDAGLQGEGITAHDMSMVKMCRGSDFEETAVARAQL 420
 QY 421 AEFTVSGVATVNGFLRALLREEDFTSKRATGTDADPHLLQAPPADDEQGRILDLYADV 480
 Db 421 AEFTVSGVATVNGFLRALLREEDFTSKRATGTDADPHLLQAPPADDEQGRILDLYADV 480
 QY 481 TVNKPHGFPKDKVAPIDKLPNKLDPURGSSDRKLQKGPAFAFARDLREQLAVDIT 540
 Db 481 TVNKPHGFPKDKVAPIDKLPNKLDPURGSSDRKLQKGPAFAFARDLREQLAVDIT 540
 QY 601 LREAMPVNQIQLLRGRTVTPYPSVCRFKEAASGVDIFRLFDALNDNSQMRPA 660
 Db 601 LREAMPVNQIQLLRGRTVTPYPSVCRFKEAASGVDIFRLFDALNDNSQMRPA 660
 QY 661 IDAVLENTNTAVAVAMYSGDLSDPNKRKYLYDYLKMAEEVKSRAHILAKDMAGLLR 720

XX
 Db 661 IDAVLENTNTAVAVAMYSGDLSDPNKRKYLYDYLKMAEEVKSRAHILAKDMAGLLR 720
 XX
 QY 721 PAAVTKVLTALRREFDLPVHVTHTDAGGOLATVAAQAGADAVDGAAPLSGTTSQPS 780
 Db 721 PAAVTKVLTALRREFDLPVHVTHTDAGGOLATVAAQAGADAVDGAAPLSGTTSQPS 780
 XX
 QY 781 LSATVAFAAHTTRDGTGSLBASDDEPYWAVRGXYLPRFGTGPCTGVRHPEPGQOL 840
 Db 781 LSATVAFAAHTTRDGTGSLBASDDEPYWAVRGXYLPRFGTGPCTGVRHPEPGQOL 840
 XX
 QY 841 SNLRAQATGLGLADRELIEDNYAVNEMGRPWTPSKVKWGDALHLVGAWDPAF 900
 Db 841 SNLRAQATGLGLADRELIEDNYAVNEMGRPWTPSKVKWGDALHLVGAWDPAF 900
 XX
 QY 901 AADPKYDIDSVIAFLRGLGEIYKNGPWWPLRERLEGSEGAPELTVPEERQAHIDA 960
 Db 901 AADPKYDIDSVIAFLRGLGEIYKNGPWWPLRERLEGSEGAPELTVPEERQAHIDA 960
 XX
 QY 961 DDSKERRNSLNRLLEPKPTEFLHRRRGNTSALADDREFFYGLVEGRETILRIPDVRT 1020
 Db 961 DDSKERRNSLNRLLEPKPTEFLHRRRGNTSALADDREFFYGLVEGRETILRIPDVRT 1020
 XX
 QY 1021 LLVRDIAISEPDDKMRNTVANVNGIORMVRURRSVSYTATAEKASNSNKHVAFFA 1080
 Db 1021 LLVRDIAISEPDDKMRNTVANVNGIORMVRURRSVSYTATAEKADSSNKHVAFFA 1080
 XX
 QY 1081 GVVTTWAGSDEVAGDVALIEMKMEITASWDGKDRVWPAATKVEGDLIIVS 1140
 Db 1081 GVVTTWAGSDEVAGDVALIEMKMEITASWDGKDRVWPAATKVEGDLIIVS 1140
 XX
 QY 1101 GVVTTWAGSDEVAGDVALIEMKMEITASWDGKDRVWPAATKVEGDLIIVS 1140

RESULT 2

AAB67129

ID AAB67129 standard; Protein; 1140 AA.

XX

AC AAB67129;

XX

DT 12-APR-2001 (first entry)

DE Corynebacterium glutamicum

XX

KW Pyruvate carboxylase; anaplerotic pathway; industrial fermentation;

XX

KW oxaloacetate.

XX

Corynebacterium glutamicum.

XX

US6171833-B1.

XX

PD 09-JAN-2001.

XX

PF 23-DEC-1998; 98US-0220081.

XX

PR 23-DEC-1998; 98US-0220081.

XX

(MAST) MASSACHUSETTS INST TECHNOLOGY.

XX

PA Sinskey AJ, Lessard PA, Willis LB;

XX

DR WPI; 2001-122330/13.

DR N-PSDB; AAF32165.

XX

PT Novel nucleic acid encoding pyruvate carboxylase from *Corynebacterium*

PT glutamicum, for replenishing oxaloacetate consumed during lysine and

PT glutamic acid production in industrial fermentations -

XX

CC The present invention provides the protein and coding sequences of the

CC *Corynebacterium glutamicum* pyruvate carboxylase protein. This is an

CC enzyme in the anaplerotic pathway. It can be used in the replenishment of

CC oxaloacetate consumed during lysine and glutamic acid production in

CC industrial fermentation.

XX	Sequence	1140 AA:	Db	961 DDSKERRNSLNRLLPFPKPTEEFLIRRFRGNTSALLDRFFYGLVREGTIRLLEDVRIP 1020
Query	Match	100.0% Score 5788; DB 22; length 1140;	Qy	1021 LLVRDAISESPDKGKMRNVVANVNGQIRPVRVRSVSESTATAKADSSNKHWAPFA 1080
Best Local Similarity	100.0% Pred. No. 0;	Mismatches 0; Indels 0; Gaps 0;	Db	1021 LLVRDAISESPDKGKMRNVVANVNGQIRPVRVRSVSESTATAKADSSNKHWAPFA 1080
Matches	1140; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	Qy	1 MSHHSSTLPAFKKILVANRGEIARAFRALETAEGATVAYPRDRGSFHRSEAVR 60
Db	1 MSHHSSTLPAFKKILVANRGEIARAFRALETAEGATVAYPRDRGSFHRSEAVR 60	Qy	1 MSHHSSTLPAFKKILVANRGEIARAFRALETAEGATVAYPRDRGSFHRSEAVR 60	
Qy	61 IGTGESPVKAFLDIBIGAKKVKADATYPGYGFLSENQALARCAENGTIFGPTPEV 120	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	61 IGTGESPVKAFLDIBIGAKKVKADATYPGYGFLSENQALARCAENGTIFGPTPEV 120	Qy	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Qy	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSABGQTYIFVKAVAGGGGRGMF 180	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSABGQTYIFVKAVAGGGGRGMF 180	Qy	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSABGQTYIFVKAVAGGGGRGMF 180	
Qy	181 VASDELRLKATEASREAAFGDCAVYVERAVINPOHTEVOLGDHTCEVHLYERDGS 240	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	181 VASDELRLKATEASREAAFGDCAVYVERAVINPOHTEVOLGDHTCEVHLYERDGS 240	Qy	181 VASDELRLKATEASREAAFGDCAVYVERAVINPOHTEVOLGDHTCEVHLYERDGS 240	
Qy	241 LQRHOKVVEIAPQHDLPELDRICADAVKFCRSIGYOGAGTVEFLVNEKGNTVIEEN 300	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	241 LQRHOKVVEIAPQHDLPELDRICADAVKFCRSIGYOGAGTVEFLVNEKGNTVIEEN 300	Qy	241 LQRHOKVVEIAPQHDLPELDRICADAVKFCRSIGYOGAGTVEFLVNEKGNTVIEEN 300	
Qy	301 PRQVEHTTEEVTDVLQKAQMULAGATLKEGLTQDKIKTHGALOCRITEDPNNG 360	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	301 PRQVEHTTEEVTDVLQKAQMULAGATLKEGLTQDKIKTHGALOCRITEDPNNG 360	Qy	301 PRQVEHTTEEVTDVLQKAQMULAGATLKEGLTQDKIKTHGALOCRITEDPNNG 360	
Qy	361 FRPDGTITAYRSPGGAGYGRUDGAQALGEGITAHDMSMVKMTGRGSDTETAVARAQL 420	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	361 FRPDGTITAYRSPGGAGYGRUDGAQALGEGITAHDMSMVKMTGRGSDTETAVARAQL 420	Qy	361 FRPDGTITAYRSPGGAGYGRUDGAQALGEGITAHDMSMVKMTGRGSDTETAVARAQL 420	
Qy	421 AEFTVSGVATNIGFLRALLREEDFTSKRATGFADPHPLQAPADDQGRDQRLDLYAV 480	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	421 AEFTVSGVATNIGFLRALLREEDFTSKRATGFADPHPLQAPADDQGRDQRLDLYAV 480	Qy	421 AEFTVSGVATNIGFLRALLREEDFTSKRATGFADPHPLQAPADDQGRDQRLDLYAV 480	
Qy	481 TUNKPHGVKRKDVAPIDKLPLKPLGSRRLQKGPAAARDLQRDQALAVDTT 540	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	481 TUNKPHGVKRKDVAPIDKLPLKPLGSRRLQKGPAAARDLQRDQALAVDTT 540	Qy	481 TUNKPHGVKRKDVAPIDKLPLKPLGSRRLQKGPAAARDLQRDQALAVDTT 540	
Qy	541 FRDAHQSLLATRVSFALEAVAKLPELPSVEAWGSGATYDVAMRLFEDWDRDLE 600	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	541 FRDAHQSLLATRVSFALEAVAKLPELPSVEAWGSGATYDVAMRLFEDWDRDLE 600	Qy	541 FRDAHQSLLATRVSFALEAVAKLPELPSVEAWGSGATYDVAMRLFEDWDRDLE 600	
Qy	601 LREAMPVNVIQMLLGRGRNTVGYTYPDSDTCRAFTKEAASSGVDFRIFEAFLNDYQSMPRA 660	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	601 LREAMPVNVIQMLLGRGRNTVGYTYPDSDTCRAFTKEAASSGVDFRIFEAFLNDYQSMPRA 660	Qy	601 LREAMPVNVIQMLLGRGRNTVGYTYPDSDTCRAFTKEAASSGVDFRIFEAFLNDYQSMPRA 660	
Qy	661 IDAVLETNTAVAEVAMAYGSDLSPNPKIYLTDLYKMAEETVSGAHLAIKOMAGLR 720	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	661 IDAVLETNTAVAEVAMAYGSDLSPNPKIYLTDLYKMAEETVSGAHLAIKOMAGLR 720	Qy	661 IDAVLETNTAVAEVAMAYGSDLSPNPKIYLTDLYKMAEETVSGAHLAIKOMAGLR 720	
Qy	721 PAATVTKLVALRREDFLPVHVTHTAGGOLATVAAQAGADAVGASAPLGTTSQDS 780	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	721 PAATVTKLVALRREDFLPVHVTHTAGGOLATVAAQAGADAVGASAPLGTTSQDS 780	Qy	721 PAATVTKLVALRREDFLPVHVTHTAGGOLATVAAQAGADAVGASAPLGTTSQDS 780	
Qy	781 LSATVAAFAHTRDRDGLSLEAVSDLEPYHEAVRSLYLPFESGTGPCTGTVRYRHEPFGOL 840	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	781 LSATVAAFAHTRDRDGLSLEAVSDLEPYHEAVRSLYLPFESGTGPCTGTVRYRHEPFGOL 840	Qy	781 LSATVAAFAHTRDRDGLSLEAVSDLEPYHEAVRSLYLPFESGTGPCTGTVRYRHEPFGOL 840	
Qy	841 SNLRAQATLGLADLPELQEDNYAVNEMGGRPKVTPSKWQDALLHVGADYDPAF 900	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	841 SNLRAQATLGLADLPELQEDNYAVNEMGGRPKVTPSKWQDALLHVGADYDPAF 900	Qy	841 SNLRAQATLGLADLPELQEDNYAVNEMGGRPKVTPSKWQDALLHVGADYDPAF 900	
Qy	901 AADPQKYDPPSVTAFLRSLGNPGWPRLTRALESGEKGAPLVEPEOAHLD 960	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Db	901 AADPQKYDPPSVTAFLRSLGNPGWPRLTRALESGEKGAPLVEPEOAHLD 960	Qy	901 AADPQKYDPPSVTAFLRSLGNPGWPRLTRALESGEKGAPLVEPEOAHLD 960	
Qy	961 DDSKERRNSLNRLLPFPKPTEEFLIRRFRGNTSALLDRFFYGLVREGTIRLLEDVRIP 1020	Db	1081 GWVTTVAEDEVKAGDAVIAEAMKMEITASDGKIDRVVPPATKVEGGDLIVWS 1140	
Qy	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSACGQTYIFVKAVAGGGGRGMF 180	Qy	121 LDLTGDKSRAVTAKKAGLPVLAESTPSKNIETVKSACGQTYIFVKAVAGGGGRGMF 180	

Db	121	LDLTGDKSRVAAKAKGLPVLAEESTPSKNDTEIVKSAEGTYPIFKAVAGGGGRMF	180	27-AUG-2002 (first entry)
QY	181	VASPDRLKLTAEAREAAFGDGAIVVERAVINPOHIEVILGDTGEVHLYERDCS	240	Corynebacterium wild-type feedback-resistant pyruvate carboxylase enzyme.
Db	181	VASPDRLKLTAEAREAAFGDGAIVVERAVINPOHIEVILGDTGEVHLYERDCS	240	Feedback-resistant; pyruvate carboxylase; enzyme;
QY	241	LQRHQKVVEITAPAOHLDPELDRTRCAADYKFCRSICGQAGTVEFLDKEGNHVFLEMN	300	aspartic acid feedback inhibition resistant.
Db	241	LQRHQKVVEITAPAOHLDPELDRTRCAADYKFCRSICGQAGTVEFLDKEGNHVFLEMN	300	Corynebacterium glutamicum.
QY	301	PRIOEHETVVEETVTDLVKAQMRLAAGATKELSIQDQKTHGALQCRITTEPDNG	360	
Db	301	PRIOEHETVVEETVTDLVKAQMRLAAGATKELSIQDQKTHGALQCRITTEPDNG	360	
QY	361	FRPDGTITAYRSPGAGVRLDGAQOLGGETAHFDSMLVMTGCRSDFETAVARQAL	420	
Db	361	FRPDGTITAYRSPGAGVRLDGAQOLGGETAHFDSMLVMTGCRSDFETAVARQAL	420	
QY	421	AEFTVSGVATNIGFTRALLBEEDEFSKRATGFTADPHLQAPADDEQGRILDLADY	480	
Db	421	AEFTVSGVATNIGFTRALLBEEDEFSKRATGFTADPHLQAPADDEQGRILDLADY	480	
QY	481	TVNKGHGVRSKDVAAPIDKLPLNPKDQPLPGRSDLQKOLGPAAFRDLREGDADYDT	540	
Db	481	TVNKGHGVRSKDVAAPIDKLPLNPKDQPLPGRSDLQKOLGPAAFRDLREGDADYDT	540	
QY	541	FRDAHQSLATRVSFALKAAEAKLTPELSEAWGGATYDAMRFLEFDPRDLDE	600	
Db	541	FRDAHQSLATRVSFALKAAEAKLTPELSEAWGGATYDAMRFLEFDPRDLDE	600	
QY	601	LREAMPVNQIQLRGRNTVGYTPPDVSCRAFVIEAASSGVDTRIFDALNDVSMRPA	660	
Db	601	LREAMPVNQIQLRGRNTVGYTPPDVSCRAFVIEAASSGVDTRIFDALNDVSMRPA	660	
QY	661	IDAVENTNTAAVEAMAYSGDLSIDSPNEKLYTDYLLKMASBIVKGAGHTIAKDMAGLLR	720	
Db	661	IDAVENTNTAAVEAMAYSGDLSIDSPNEKLYTDYLLKMASBIVKGAGHTIAKDMAGLLR	720	
QY	721	PAAVTKLVIAFLRREDFLPVHHTDHTAGSOLATYAAQGADAGASAPLSTSQPS	780	
Db	721	PAAVTKLVIAFLRREDFLPVHHTDHTAGSOLATYAAQGADAGASAPLSTSQPS	780	
QY	781	LSATWAAFAHTRDTGSLSEAVSDELPYEAWRGKYLPEFSGTPOPTGRYRHEPGQL	840	
Db	781	LSATWAAFAHTRDTGSLSEAVSDELPYEAWRGKYLPEFSGTPOPTGRYRHEPGQL	840	
QY	841	SNLRAQATAGLADREFELLEDNYAVNEMGRPTKVTSPSSKVGDLALHLYGADPAF	900	
Db	841	SNLRAQATAGLADREFELLEDNYAVNEMGRPTKVTSPSSKVGDLALHLYGADPAF	900	
QY	901	AADPKYDIDPSVTAFLRGLPGLNPFGGWPEPLRPALEGRSEGKAPLVEPEECAHDLA	960	
Db	901	AADPKYDIDPSVTAFLRGLPGLNPFGGWPEPLRPALEGRSEGKAPLVEPEECAHDLA	960	
QY	961	DDSKERRNLNRLPKPKEEFLRRRREGNTSALDDREFYGVLEGRPLRIPDRPT	1020	
Db	961	DDSKERRNLNRLPKPKEEFLRRRREGNTSALDDREFYGVLEGRPLRIPDRPT	1020	
QY	1021	LLYRDLAISEPDKGKMRNUNVANVQIQRMVRDRESVESVATAEKADSSNKHWAAPFA	1080	
Db	1021	LLYRDLAISEPDKGKMRNUNVANVQIQRMVRDRESVESVATAEKADSSNKHWAAPFA	1080	
QY	1081	GVVTVTVAEGDEVKGDAVIALEAMKMEITASWDGKIDRVVVFAATKVEGGDLIVVS	1140	
Db	1081	GVVTVTVAEGDEVKGDAVIALEAMKMEITASWDGKIDRVVVFAATKVEGGDLIVVS	1140	
RESULT 4				
AAU98053				
ID	AAU98053	standard; Protein; 1140 AA.		
XX				
AAU98053;				

QY	541 FRDAHQSLATRVRSEALKPAEAVALTPELLEVAANGATYDVAARLFEDPWDRLDE 600	PT Increasing microbial production of specific amino acids by
Db	542 FRDAHQSLATRVRSEALKPAEAVALTPELLEVAANGATYDVAARLFEDPWDRLDE 601	PT Increasing activity or expression of pyruvate carboxylase
QY	601 LREAMPNVNTQMLLRGRNTVGTYPYPSVCRAFKEAASSGVDIFRFDALNDYSQMRPA 660	XX
Db	602 LREAMPNVNTQMLLRGRNTVGTYPYPSVCRAFKEAASSGVDIFRFDALNDYSQMRPA 661	CC
QY	661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLVYKMAERIVKGSHILAIKDMAGLRL 720	CC
Db	662 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLVYKMAERIVKGSHILAIKDMAGLRL 721	CC
QY	721 PAAVTKLVTALARREDFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780	CC
Db	722 PAAVTKLVTALARREDFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 781	CC
QY	781 LSAIVAAFAHTRRTDTGLSLEAVSDLEIYWEAVRLYLPFESCTPGPGVRHIEPGQL 840	CC
Db	782 LSAIVAAFAHTRRTDTGLSLEAVSDLEIYWEAVRLYLPFESCTPGPGVRHIEPGQL 841	CC
QY	841 SNLRAQATLAGLADRFELIEDNYAAVNEMMLGRPTKVPSKVGVDIALHLYGAVDPAF 900	CC
Db	842 SNLRAQATLAGLADRFELIEDNYAAVNEMMLGRPTKVPSKVGVDIALHLYGAVDPAF 901	CC
QY	901 AADPKDIDPSVTAFLRGELGNPGWPPEPLTRALEGRSGKAPLTVFEEQAHDLA 960	CC
Db	902 AADPKDIDPSVTAFLRGELGNPGWPPEPLTRALEGRSGKAPLTVFEEQAHDLA 961	CC
QY	961 DDKERKNSLNLLFPLPKPTEELERHRFRFGNSALDREFFYGLVKGRETLRLPVRTP 1020	CC
Db	962 DDKERKNSLNLLFPLPKPTEELERHRFRFGNSALDREFFYGLVKGRETLRLPVRTP 1021	CC
QY	1021 LLVRDAAISEPDKGKMRNVAWNGQIRPMVRDRSVESTVATAEKDSNKGHVAPEA 1080	CC
Db	1022 LLVRDAAISEPDKGKMRNVAWNGQIRPMVRDRSVESTVATAEKDSNKGHVAPEA 1081	CC
QY	1081 GIVWTWTAEGDVKAGDAVATEAMMEATATSVQKDRWVVPATKPGGDLIVWS 1140	CC
Db	1082 GIVWTWTAEGDVKAGDAVATEAMMEATATSVQKDRWVVPATKPGGDLIVWS 1141	CC
RESULT 6		
AAW93971		
ID	AAW93971 standard; protein; 1140 AA.	
XX		
AC		
XX		
DT	30-JUN-1999 (first entry)	
XX		
DE	C. glutamicum Pyruvate carboxylase protein.	
XX		
KW	Pyruvate carboxylase; amino acid production; lysine production; threonine production; homoserine production; glutamate production; arginine production; feed additive; condiment; pharmaceutical; fine chemical; ss.	
XX		
OS	Corynebacterium glutamicum.	
XX		
DE1931609-A1.		
PD	15-APR-1999.	
XX		
PF	14-JUL-1998; 98DE-1031609.	
XX		
PR	04-OCT-1997; 97DE-1043894.	
XX		
PA	(KERJ) FORSCHUNGZENTRUM JUELICH GMBH.	
XX		
PI	Eikmanns B, Peters-Wendisch P, Sahn H;	
XX		
DR	WPI: 1999-24551/21.	
XX		
N-PSDB; AAX24102.		
QY	601 LREAMPNVNTQMLLRGRNTVGTYPYPSVCRAFKEAASSGVDIFRFDALNDYSQMRPA 660	CC
Db	601 LREAMPNVNTQMLLRGRNTVGTYPYPSVCRAFKEAASSGVDIFRFDALNDYSQMRPA 660	CC
QY	661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLVYKMAERIVKGSHILAIKDMAGLRL 720	CC
Db	661 IDAVLENTTAVAEVAMAYSDLSDPNEKLYTDLVYKMAERIVKGSHILAIKDMAGLRL 720	CC
QY	721 PAAVTKLVTALARREDFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780	CC
Db	721 PAAVTKLVTALARREDFDLPVHVTHTAGGOLATYFAAQAGADAVGASAPLSQTSSQPS 780	CC

QY	781	LSAIYAAFAHTARDTGSLAEVDLSELEYWEAVRGLYVLFPESTCPGPGVRYHEIGQQL	841
Db	781	LSAIYAAFAHTARDTGSLAEVDLSELEYWEAVRGLYVLFPESTCPGPGVRYHEIGQQL	841
Db	781	SNRQAQATALGLADRFELIEDYAAVNEMLGRPTKWPSSKVGDDALHLHVGADPADE	841
Db	781	SNRQAQATALGLADRFELIEDYAAVNEMLGRPTKWPSSKVGDDALHLHVGADPADE	841
Qy	901	AADPOKQDIPDSVIAFLRGELGNPPGCGWPEPLRTRALEGRSBGKALPTEVPEEEQHQLDA	960
Qy	901	AADPOKQDIPDSVIAFLRGELGNPPGCGWPEPLRTRALEGRSBGKALPTEVPEEEQHQLDA	960
Qy	961	DISKERNSLNLLPKPTTELEHRRRFGNTSALDREFFYGLVCEGRETILRLPYRTP	1021
Db	961	DISKERNSLNLLPKPTTELEHRRRFGNTSALDREFFYGLVCEGRETILRLPYRTP	1021
Db	961	DDSKERRNSLNRLLPKPTTELEHRRRFGNTSALDREFFYGLVCEGRETILRLPYRTP	1021
Qy	1021	LLVRDAAISEPDGKGMNVANVNGQIRPMYRDRDSESVTRAAKADSSNKGHVAAPFA	1081
Qy	1021	LLVRDAAISEPDGKGMNVANVNGQIRPMYRDRDSESVTRAAKADSSNKGHVAAPFA	1081
Db	1021	GVVTVTVVAGDEVKAGDAVAAIEAMKMEATITASVGDCKIDRVVWPAATKVEGGDLVVWS	1101
Qy	1081	GVVTVTVVAGDEVKAGDAVAAIEAMKMEATITASVGDCKIDRVVWPAATKVEGGDLVVWS	1101
Db	1081	GVVTVTVVAGDEVKAGDAVAAIEAMKMEATITASVGDCKIDRVVWPAATKVEGGDLVVWS	1101
RESULT 7			
AA93249	AA93249	standard; protein: 1140 AA.	
AC	AA93249;		
XX			
DT	26-SEP-2001	(first entry)	
DE	C glutamicum	protein fragment mutant P458S.	
XX			
KW	Coryneform bacterium; amino acid synthesis; vitamin; saccharide;		
KW	organic acid synthesis; mutant; mutein.		
XX			
OS	Corynebacterium glutamicum.		
OS	Synthetic.		
XX			
FH		Location/Qualifiers	
FT		Misc-difference 458	
FT		/note= "wild-type Pro substituted by Ser"	
XX			
PN	EPI108790-A2.		
XX			
PD	20-JUN-2001.		
XX			
PF	18-DEC-2000; 2000EP-0127688.		
XX			
PR	16-DEC-1999; 99JP-037784.		
PR	07-APR-2000; 2000JP-0159162.		
PR	03-AUG-2000; 2000JP-0280988.		
XX			
PA	(KYOW) KYOWA HAKKO KOGYO KK.		
XX			
PI	Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;		
PI	Tateishi N, Senoh A, Ikeda M, Ozaki A;		
DR	WPI; 2001-376931/40.		
XX			
PT	Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene		
PT	Claim 43; Page :- 246pp + Sequence Listing; English.		
XX			
CC	The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium <i>Corynebacterium glutamicum</i> . These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and		
CC	expression profile or pattern of a gene and identifying homologous gene		
XX			

QY 661 IDAVLENTNAAEVAMAYSGDSLSPNEKLYTLDYKLMAMEEIVKSGAHTLAIKOMAGLR 720
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 QY 721 PAAYTKLVALRREDFLPYHVTHTDAGGOLATYFAAACAGADAVDAGASAPLSGNTSOP 780
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 721 PAAYTKLVALRREDFLPYHVTHTDAGGOLATYFAAACAGADAVDAGASAPLSGNTSOP 780
 QY 781 LSATVAFAAHTRRDRGSLSEASDLEPYEAWRGYLPESGTGCTGVRHETPGQL 840
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 781 LSATVAFAAHTRRDRGSLSEASDLEPYEAWRGYLPESGTGCTGVRHETPGQL 840
 QY 841 SNLRAQATLGLARFELLEDNYAANEMGRPTKVTPSSKVVGDLALHVGAGYDPAD 900
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 841 SNLRAQATLGLARFELLEDNYAANEMGRPTKVTPSSKVVGDLALHVGAGYDPAD 900
 QY 901 AADPQYDIDPSVTAFLRGELGNPGWPGPLRTRALESEGKAPLVEPEESOAHLLA 960
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 901 AADPQYDIDPSVTAFLRGELGNPGWPGPLRTRALESEGKAPLVEPEESOAHLLA 960
 QY 961 DDSKERRNSLNRLLEPKPTEFLEHRRFGNTSALDDREPFYGLVEGRERLIRLDPVRP 1020
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 961 DDSKERRNSLNRLLEPKPTEFLEHRRFGNTSALDDREPFYGLVEGRERLIRLDPVRP 1020
 QY 1021 LLVRDAISESPDDKGMRNWNVANNGQIRPMVRDRSVESTATAEKADSSNKGHVAAPFA 1080
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 1021 LLVRDAISESPDDKGMRNWNVANNGQIRPMVRDRSVESTATAEKADSSNKGHVAAPFA 1080
 QY 1081 GVVTVVAEDEVKAGDAVATEAMKMEATITASVGDKIDRVVVAATKVEGGDLIVVS 1140
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 1081 GVVTVVAEDEVKAGDAVATEAMKMEATITASVGDKIDRVVVAATKVEGGDLIVVS 1140

RESULT 9

QY AAU98050 standard: Protein; 1157 AA.

XX AAU98050:

XX 27-AUG-2002 (first entry)

XX Corynebacterium feedback-resistant pyruvate carboxylase enzyme.

XX Feedback-resistant: Pyruvate carboxylase; enzyme;

KW aspartic acid feedback inhibition resistant.

XX Corynebacterium glutamicum.

XX Key Location/Qualifiers

FT 1..18 /note= "Specifically claimed in claim 18"

FT 154..176 /note= "Specifically claimed in claim 18"

FT 193..205 /note= "Specifically claimed in claim 18"

FT 217..229 /note= "Specifically claimed in claim 18"

FT 238..250 /note= "Specifically claimed in claim 18"

FT Region 466..478 /note= "Specifically claimed in claim 18"

FT Region 18..APR-2002. /note= "Specifically claimed in claim 18"

XX WO200231158-A2.

XX 12-OCT-2001; 2001WO-US31893.

PR 13-OCT-2000; 2000US-239913P.

XX (ARCH) ARCHER - DANIELS MIDLAND CO.

PA PI Hanke PD;

XX Sequence 1157 AA;

Query Match 99.5%; Score 5759; DB 23; Length 1157;

Best Local Similarity 99.4%; Pred. No: 0;

Matches 1133; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSHHGSTLPAFKKLIVANRGEIARAFRAALEGCAATVLYPRDRGSFHSRFASEAVR 60
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 AC 18 VSTHTHSSTLPAFKKLIVANRGEIARAFRAALEGCAATVLYPRDRGSFHSRFASEAVR 77

DB 61 IGTESSPVKAVALDIBIGAKKVKADAIYPGGLSENNOLARCAENGITFIGPTPEV 120
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR 78 IGTESSPVKAVALDIBIGAKKVKADAIYPGGLSENNOLARCAENGITFIGPTPEV 137
 QY 121 LDLTGDKRSRAVTAKKAGLPVLAESTPSKNIDEIKSAEGOTYPIFVKAVAGGGRMRF 180
 DB 138 LDLTGDKRSRAVTAKKAGLPVLAESTPSKNIDEIKSAEGOTYPIFVKAVAGGGRMRF 197

QY 181 VASPDILRKIATEAREEAEAFGDRAVYVERAVINPOHIVIOLGDDHTGTEVHVLERDCS 240
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR 198 VSSPDLERLKIATEAREEAEAFGDSVYVERAVINPOHIVIOLGDDHTGTEVHVLERDCS 257

QY 241 LQRRIKVKVETAPQHLDPELDRICADAYKFCRSIGYQAGATVFLDKGHNFIEMN 300
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 DR 258 LQRRIKVKVETAPQHLDPELDRICADAYKFCRSIGYQAGATVFLDKGHNFIEMN 317

QY 301 PRIQVHTVVEVTEVTDLVAQMRQAGATIKEGLTQDKIKTHAQLQRITDPNNG 360
 DB 318 PRIQVHTVVEVTEVTDLVAQMRQAGATIKEGLTQDKIKTHAQLQRITDPNNG 377

QY 361 FRPDPGTTATYRSPSGAGVRLDGAQIGGETTAHDMSLWYKMTCHGSDFETAVARQRAL 420
 DR 378 FRPDPGTTATYRSPSGAGVRLDGAQIGGETTAHDMSLWYKMTCHGSDFETAVARQRAL 437

QY 421 AEFTSGVATMIGFRLRREDFSKRITGFDHDPHQLQAPPADDEGRLYLADY 480
 DB 438 AEFTSGVATMIGFRLRREDFSKRITGFDHDPHQLQAPPADDEGRLYLADY 497

QY 481 TVNKGIGVRPKDVAAPIDKLPNIKOLPLPGRSDRQLQPAFADRLREODALAVTDT 540
 DB 498 TVNKGIGVRPKDVAAPIDKLPNIKOLPLPGRSDRQLQPAFADRLREODALAVTDT 557

QY 541 FRDAIOSLAVRVRSEFALKPAEAVAKLTBLLSVAWGGATYDVAARLFEDPDRDLE 600
 XX ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db	558	FRDAHQSSLATRVHSFAKPKAAEAVAKITPELSSVEAGGATYDVAARFLFPWDRIDE	617	XX	Proteins and their DNA useful for microbial production of L-amino acids
Qy	601	LREAMPNVNQMLLRGRNNGVYTPYDPSVSCRAFYKEAASSGVDFRIFRDALNDVSQMRPA	660	PT	-
Db	613	LREAMPNVNQMLLRGRNNGVYTPYDPSVSCRAFYKEAASSGVDFRIFRDALNDVSQMRPA	677	XX	Claim 9; Page 132-135; 215pp; Japanese.
Qy	661	IDAVLETTNAEVAEYAMAXSGDLSDPNEKXLTIDYLKMAEYVKGSAHILAKDMAGLR	720	XX	The present sequence is provided in a specification relating to genes
Db	678	IDAVLETTNAEVAEYAMAXSGDLSDPNEKXLTIDYLKMAEYVKGSAHILAKDMAGLR	737	CC	encoding thermophilic amino acid biosynthesis system enzymes of
Qy	722	PAAVTKLYVALRREFDLPVPHVHHTDAGGQLATYFAAQAGADAVDGASAPLSGTTSQPS	780	CC	the thermophilic bacterium <i>Corynebacterium</i> thermomaminogenes.
Db	738	PAAVTKLYVALRREFDLPVPHVHHTDAGGQLATYFAAQAGADAVDGASAPLSGTTSQPS	797	CC	The novel proteins retain at least 30% isocitrate ligase activity
Qy	781	LSATVAFAHTTRDGTLSLEAVSDLEPWWEAVRGLYLPFESGTGGPTGRVYRHEIPGSQL	840	CC	after heating at 50°C for 5 minutes. DNA fragments encoding the
Db	798	LSATVAFAHTTRDGTLSLEAVSDLEPWWEAVRGLYLPFESGTGGPTGRVYRHEIPGSQL	857	CC	enzymes were isolated from a <i>Corynebacterium</i> thermomaminogenes
Qy	841	SNRQAQATAGLADRFELIEDNTAATVNLGRPTKVPSSKGVDLALHVGAGVDPDF	900	CC	chromosomal DNA plasmid library by PCR. The DNA may be used for
Db	858	SNRQAQATAGLADRFELIEDNTAATVNLGRPTKVPSSKGVDLALHVGAGVDPDF	917	XX	developing strains of amino acid producing microorganisms.
Qy	901	AADPOKYDIPDSYTAFLERGELGNPGGMPPEPLTRALEGRSGKAPLTPEEEQAMIDA	960	CC	XX
Db	918	AADPOKYDIPDSYTAFLERGELGNPGGMPPEPLTRALEGRSGKAPLTPEEEQAMIDA	977	CC	Sequence 1139 AA;
Qy	961	DDSKERRNSLNLFLPKPTEEFLEHRRRGNTSALDREFEFGVLVEGRETLIRLPDVRTP	1020	Qy	Query Match 91.6%; Score 5302.5; DB 22; Length 1139;
Db	978	DDSKERRNSLNLFLPKPTEEFLEHRRRGNTSALDREFEFGVLVEGRETLIRLPDVRTP	1037	Db	Best Local Similarity 91.0%; Pred. No. 0; Matches 1036; Conservative 43; Mismatches 58; Indels 1; Gaps 1;
Qy	1021	LLVRDAAISEPDKGMRANVANNGQIRPMVRDVSVESTAAEKADSNSKGHVAAPFA	1080	Qy	3 TMSSTLPAFKKLYVANRGEIAVRAFRAALETGAAVTAIPREDRSFSFRHFASEVRIG 62
Db	1038	LLVRDAAISEPDKGMRANVANNGQIRPMVRDVSVESTAAEKADSNSKGHVAAPFA	1097	Db	3 TMSSTLPAFKKLYVANRGEIAVRAFRAALETGAAVTAIPREDRSFSFRHFASEVRIG 62
Qy	1081	GVVTVTVAEGDEVKAGDAWVATEAMKHEATIPASDCKIDRVWPAATKVEGDLIVWS	1140	Qy	123 LTGDKSKRAVTAKKAGLFLVLAESTSPSKNIDEITVSKAAGOTYPIFVVAAGGGGRMRFVA 182
Db	1098	GVVTVTVAEGDEVKAGDAWVATEAMKHEATIPASDCKIDRVWPAATKVEGDLIVWS	1157	Db	123 LTGDKSKRAVTAKKAGLFLVLAESTSPSKNIDEITVSKAAGOTYPIFVVAAGGGGRMRFVA 182
RESULT 10				Qy	183 SDDELKILATEASREAAFRAAFGDAVVERAVINPOHEVOTLGDHGEVWHLYERDCSIO 242
AAB83180				Db	183 KPDRELAREASREAAFAGDGSVYVERAVIKPQIIEVQIJDHGWDVHLYERDCSIO 242
ID AAB83180				Qy	243 RRHKVVEIAPAQHUEPELRICADAVFKCRSIGQAGTVEFLDEKGHNHFEMNPR 302
XX				Db	243 RRHKVVEIAPAQHUEPELRICADAVFKCRSIGQAGTVEFLDEKGHNHFEMNPR 302
AC AAB83180;				Qy	303 IQEHTVTEEVYDVLVKAQMLAAGATLKEGLTQDOKIKTHGAALQCRITTEDPNNGR 362
XX				Db	303 IQEHTVTEEVYDVLVKAQMLAAGATLKEGLTQDOKIKTHGAALQCRITTEDPNNGR 362
DT 09-JUL-2001 (first entry)				Qy	363 PDTGTGTTAYRSPGGAVRVLQDGAQOLGEITAHFDSDMVLKMCRGSDDETAVSRARALAE 422
XX				Db	363 PDTGTGTTAYRSPGGAVRVLQDGAQOLGEITAHFDSDMVLKMCRGSDDETAVSRARALAE 422
DE Corynebacterium thermoaminogenes pc protein.				Qy	423 FTVSGVATNIGFLRALLREEDFTSKRATGFIADPHLQAPPADEGQGRIDLVDATV 482
XX				Db	423 FTVSGVATNIGFLRALLREEDFTSKRATGFIADPHLQAPPADEGQGRIDLVDATV 482
OS Corynebacterium thermoaminogenes.				Qy	483 NPKPHGRPKDVAAPIDKLPLNPKDLPFLPRGSDRDLKQLGPAFARDLREQDALAVDTTFR 542
XX				Db	483 NPKPHGRP-EPARPIKPEVNTPLPRGSDRDLKQLGPEGFARDLREQDALAVDTTFR 541
PN WO200125447-A1.				Qy	543 DAHQSLATRVSFAKPKAAEAVAKITPELSSVEAGGATYDVAARFLFPWDRIDE
XX				Db	542 DAHQSLATRVSFAKPKAAEAVAKITPELSSVEAGGATYDVAARFLFPWDRIDE
PD 12-APR-2001.				Qy	603 EAMPNVNQMLLRGRNNGVYTPYDPSVSCRAFYKEAASSGVDFRIFRDALNDVSQMRPAID 662
XX				Db	602 EAMPNVNQMLLRGRNNGVYTPYDPSVSCRAFYKEAASSGVDFRIFRDALNDVSQMRPAID 661
PP 04-OCT-2000; 2000WO-JP06913.				Qy	663 AVLETNTAAVAMAYSGDLSDPNEKXLTIDYLKMAEYVKGSAHILAKDMAGLRPA 722
XX				Db	662 AVLETNTAAVAMAYSGDLSDPNEKXLTIDYLKMAEYVKGSAHILAKDMAGLRPA 722
PR 04-OCT-1999; 99JP-0282716.				Qy	723 AVTKLYVALRREFDLPVPHVHHTDAGGQLATYFAAQAGADAVDGASAPLSGTTSQPSMS 782
PR 01-NOV-1999; 99JP-0311147.				Db	722 AVTKLYVALRREFDLPVPHVHHTDAGGQLATYFAAQAGADAVDGASAPLSGTTSQPSMS 781
PR 21-APR-2000; 2000JP-0120687.				WPI; 2001-3-300170/31.	"
PA (AJIN) AJINOMOTO CO INC.				DR N-PSDB; AF87437.	"

Db 378 FRPDTGTTTAYRSGAGYRIDLGAQQLGGTIAHFDSTMVKMTCRGSDPFTAVARAQRAL 437

Db 65 YLDIGEGTIDIAKRNKVDAIHPGYGFLSENTHFARRCEBGGIVFTGPKSEHLDNGFDKVA 124

Qy 421 AEFTVSGVATNIGFLRALLREEDFTSKRATGFADPHLQAPPADDQGRIDLADY 480

Db 438 AEFTVSGVATNIGFLRALLREEDFTSKRATGFADPHLQAPPADDQGRIDLADY 497

Qy 481 TVNPKPHGVPRPKDVAAPIDKLPLNPKDPLPGRSRDR 515

Db 498 TVNPKPHGVPRPKDVAAPIDKLPLNPKDPLPGRSRDR 532

RESULT 12

AAU0511 AAU0511 standard; Protein; 1148 AA.

XX AC AAU0511;

XX DT 07-SEP-2001 (first entry)

XX Bacillus subtilis pyruvate carboxylase enzyme A.

XX KW Pyruvate carboxylase A; pyCA; oxaloacetate; Escherichia;

XX I-amino acid production; fermentation.

OS Bacillus subtilis strain 168.

XX EP1092776-A1.

XX PD 18-APR-2001.

PF 05-OCT-2000; 2000EP-0121763;

XX 14-OCT-1999; 99RU-0121636.

XX PA (AJIN) AJINOMOTO CO INC.

PT Gulyatnir MM, Kozlov YI, Ptitsyn LR, Altman IB, Voroshilova EB;

PT Tomantash YAV, Yampolskaya TA;

PT DR WPI; 2001-309819/33.

XX PS Claim 4; Page 17-21; 28pp; English.

XX The present sequence represents *Bacillus subtilis* pyruvate carboxylase enzyme A. The pyCA gene encodes for pyruvate carboxylase which catalyses the carboxylation of pyruvate to form oxaloacetate. Transformation of the *Bacillus subtilis* pyCA gene into a bacterium belonging to the genus *Escherichia* results in the bacterium showing L-amino acid productivity. The invention provides a novel method for producing an L-amino acid by fermentation. The method involves cultivating the bacterium in a medium and producing and accumulating the L-amino acid in the medium. The new bacterium harbouring the gene coding for an enzyme having pyruvate carboxylase activity is useful for producing higher concentrations of L-amino acids in vitro than prior art.

XX SQ Sequence 1148 AA;

Query Match 43.6%; Score 2524; DB 22; Length 1148; Best Local Similarity 46.0%; Pred. No. 1.1e-76; Matches 533; Conservative 166; Mismatches 392; Indels 48; Gaps 13;

Qy 11 AFKKILVARGELTAIRFRALETAETGAATVATYPREDRGSFHSFSEABVRIGTEGSPVKA 70

Db 5 STOKVLUVARGELTAIRFRALETAETGAATVATYPREDRGSFHSFSEABVRIGTEGSPVKA 64

Qy 71 YLVIDETIGAAKVKADATIYPGYGFSENQIARECAENGTFFIGTPENVIDLTGKSA 130

Db 65 YLDIGEGTIDIAKRNKVDAIHPGYGFLSENTHFARRCEBGGIVFTGPKSEHLDNGFDKVA 124

Qy 131 VTAARKAGLPEVLAEST-PSKNIDELVKSAEGQTYIPFKAVAGGGGRMRFVASPDETRK 189

Db 125 REQEKAGIPTGCGDGPATELFLAEWQGQANCYPLIKASIGGGGRMRTVSESEVKE 184

Qy 190 LATEASREAAFGDGAVVVERAVINPQHIEVQTLGDHNGEVVHLYERDCSLQRHOKV 249

Db 185 AYERAKSERKAFAFGDNEVYVEKLIENPKHIEVQIGDKQGNVWHLFERDCSVQRHOKV 244

Qy 250 EIAAHOHLDPELRTRICADAVKICRSIGYQACTVFEFLDEKGHNFEFMNRQIWRHTV 309

Db 245 EVAVSVSISLSPERLROQICEAVAVLAKKNVNINASIVEFLV-ANNEFYLEVNPQVOEHTI 303

Qy 310 TEETVTEVLVKAQMRMLANGATL-KELGITQDR-KITGHALOCRTTEDPANGPRDTG 366

Db 304 TEMITGVDIVOTQIILVAGHSLISKVWNIPEQDFTGIAQSRVITTEDPONDMDTG 363

Qy 367 TITARSPOGGAGYRLD-GAQOLGGEIAHFDMSLVMKMTGCRGSDPFTAVARAQRALAFTV 425

Db 364 KIMAYRSGGGGYGRDIGNSFQGAVITPYDLSLKVLSLTWALTFEQAAKMRNLQFERI 423

Qy 426 SGVATNIGFLRALLREEDFTSKRATGFADPHLQAPPADDQGRIDLADY 483

Db 424 RGIKTNIPPLEVNKAHKERFLGQYDTSIDTPPELFNPKOKDRGKTMLYIGNVTNGF 483

Qy 484 -----RPHGVPRPKDVAAPIDKLPLNPKDPLPGRSRDRKLQGPAFARDIREQDPLAV 536

Db 484 PGIGKKEKPAFDIPLGVKDVDOQP-----ARTGKQIDKGAEGLANNWVKEQSKL 536

Qy 537 TDTTFRDAHQSLIATRVSFALKPAEAVAKLTPELLSVEANGGAYDVAMRFLEDPWD 596

Db 537 TDTTFRDAHQSLIATRSHDLKKAINTAALWPELFMSMWMGGAFTDVAFRLKDPW 596

Qy 597 RLDDELREAMPVNQMLLGRNRNHYGIFTYPSDSVCRATVKEAASSGVDFRFLDNLNVSQ 656

Db 597 RLDLDRKVPNLFQMLRSSNVAVYQKPSVQKQASQGDVDFRFLDNLNVSQ 656

Qy 657 MPAIDAVLTIETNTAEEVAMAYSGDUDSPNEKLYTIDYLUKKAEEETVKGSHILAKDMA 716

Db 657 MPAIDAVLDTG-KVAAEAICTYGDIDKRNTRKYDLYTTSWAKEEAGAHLGKDMA 715

Qy 717 GLRRPAAVTKVPLTARREDFDLPVHVFHTDAGQLATYFAAQAGDAVGASAPLSGT 776

Db 716 GLLKQPAVEYELVASKENIDTPVHLHTDTSNGIVYMAKAVEAGYDVIDAVVSSNAGLT 775

Qy 777 SOPSLSAIVAAFAHTRTDGTLSLEASDLEPYWEARGLYLFESTPSPGPGVRHIEP 836

Db 776 SOPSASFYHAMEGNDRRPEMVGOFYELLSQWESPRKYSEFESMSKSPHTEIEHMP 835

Qy 837 GGOLSNLRAQATLAGLADRFELJEDINAVAVNEMLGRPTKVPSKSYVGDIALHYAGVD 896

Db 836 GQYSNQIQQAQKGVGLGDRWNWKEVYRVDNMGFIKVYKTPSSKVKVGDALMAYQNLIT 895

Qy 897 PADFAADPKYDIPDSVIAFLRGLCNPGGWPERPRTRALEGRSRGKAPLTVPEEE-- 953

Db 896 EKDVYERGESLDFPDSTVFLFKGNIGOPHGFPEKIQKLKGOE--PITVRPGELE 951

Qy 954 -----EOAHIDADDSSKERNLSNLLEPPTEELHRFRGNISALDREFF 1001

Db 952 PVSFEATKQEFFKEQHNLISD---ODAVAYALPVFTVFTSYGDTISLDPTPF 1007

Qy 1002 YGLVEGETLIRLIPDRTPLVRLDISEPDKGMNRVANVNGQTRPMYRDRSEVT 1061

Db 1008 YGMLTGEIEVEIERKLT-LIVLKLTSIGEPODPAFTRVYFLNGOPPREWVIKDESIKSSV 1066

Qy 1062 ATAEDASSNKGHVAAPFAGVWVTVTAE-GDEVKAGDAVATEAMKMEAITASVUGKID 1120

Db 1067 OERLKADTRNFSHIAAMPGIVKIVLAEGTKVNUKGDHLMINEAMKMETVQAPPSGT 1126

RESULT 13
 ABB47612 standard; Protein: 1146 AA.
 XX
 AC ABB47612;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Listeria monocytogenes protein #316.
 XX
 KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 KW vitamin B12; bacterial infection; disease.
 XX
 OS Listeria monocytogenes.
 PN WO200177335-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 11-APR-2001; 2001WO-FR01118.
 XX
 PR 11-APR-2000; 2000FR-0004629.
 XX
 PA (INSPN) INST PASTEUR.
 XX
 PI Bucherleser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 PI Dussurgeot O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;
 PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez Lopez N;
 PI Madueno E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
 PI Rose M, Voss H;
 XX
 PR; 2002-010914/01.
 XX
 PR Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 and prevention of Listeria and related bacterial infections, and
 PR related polypeptides -
 XX
 PS Claim 6; SEQ ID No 317; 192pp; French.
 XX
 CC The present invention relates to the genome sequence of Listeria
 CC monocytogenes EGD-e (see ABR30301). The genome sequence and fragments of
 CC it are useful for selecting probes and primers for detecting genes in L.
 CC monocytogenes and related organisms, and for studying genetic
 CC polymorphisms and other genomes. The present sequence is a protein
 CC encoded by the genome sequence of the present invention. Proteins
 CC expressed from the genome sequence are useful for raising specific
 CC antibodies, identification of L. monocytogenes and related organisms, and
 CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
 CC B12. The genome sequence and proteins encoded by it are also useful for
 CC selecting compounds that regulate gene expression and cell replication
 CC and modulate L. monocytogenes-related diseases. In addition, the genome
 CC sequence and proteins encoded by it are useful in pharmaceutical and
 CC vaccines compositions for the treatment or prevention of infections by L.
 CC monocytogenes and related organisms.
 Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/patents/pct/published_pct-sequences.
 XX
 SQ Sequence 1146 AA;

Query Match 43.1%; Score 2493; DB 23; Length 1146;
 Best Local Similarity 45.8%; Pred. No. 2.1e-174;
 Matches 526; Conservative 185; Mismatches 408; Indels 30; Gaps 11;

QY 13 KKLVLVANRGEIAYRAALETGAATVYIPRDRGSPHSRFSAEAVRIGTESSPVKATL 72
 5 KKLVLVANRGEIAYRAALETGAATVYIPRDRGSPHSRFSAEAVRIGTESSPVKATL 64

QY 1013 RLDPYRPLVRLDATESEPDQGMNRYVANNGQIRPMVRDRSYESVNTAAKADSNK 1072
 1017 ELEKRT-LLKLNSGEPEADGTRVYFELNGQPREINTODMNQYSTVARRKIDTTNP 1075

QY 1073 GHAAPFAG-WVVTVAEGDVKAGDAVATEAMKWEATIASVDKIDRVVPAKVE 1131

QY 1076 EHVATMTGSVLIQVWVKGGDSVKKGDPPLTEAMMETTQAFDGEVSSVYSDGTE 1135

QY	1132	GGDLIVWS	1140
Db	AAU33972	standard; Protein: 1147 AA.	
Db	AAU33972	AAU33972;	
Db	14-FEB-2002	(first entry)	
DE	Staphylococcus aureus	cellular proliferation protein #248.	
KW	Antisense; prokaryotic cellular proliferation protein;		
KW	antibiotic; antibacterial; drug design.		
OS	Staphylococcus aureus.		
PN	WO200170955-A2.		
XX	27-SEP-2001.		
PF	21-MAR-2001; 2001WO-US09180.		
XX	PR 21-MAR-2000; 2000US1-191078P.		
PR	23-MAY-2000; 2000US1-20848P.		
PR	26-MAY-2000; 2000US1-207127P.		
PR	23-OCT-2000; 2000US1-242578P.		
PR	27-NOV-2000; 2000US1-233625P.		
PR	22-DEC-2000; 2000US1-237931P.		
PR	16-FEB-2001; 2001US-269308P.		
PA	(ELIT-) ELITRA PHARM INC.		
PT	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;		
PT	Yamamoto RT, Xu HH;		
DR	WPI; 2001-611495/70.		
XX	N-PSSB; AAS51831.		
PT	New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -		
XX	Example 3; Seq ID No 5468; 511pp; English.		
CC	The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.		
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.		
SQ	Sequence 1147 AA;		
QY	13	KKLVANRGEAVRAFRAALITGAAATVAYPREDRGSFHSRFASEAVRICETEGSPVKAYL	72
4	KKLVANRGEAVRAFRAALITGAAATVAYPREDRGSFHSRFASEAVRICETEGSPVKAYL	63	
Db	73	DDEDEIGAAKVKYKADAIYPGGFLSNAQALRECAGNGITFIPPEPEWLDITGDKSRAVT	132
Db	64	NIERILDVAKANVADIAHPGIGFLSNEQFRRCAGKIGPHELHMDLGKVART	123
Db	133	AKKAGLPVL-AESTPSKNIDEIVKSAEGQTIPFVKAVAGGGGRQMRFVASPDELRKLA	191
Db	124	TAIKADLPVIGTGTGDPKISYKSELAKBFAEEAGPPLMKATSGGGKGKMRIVFRESELEDAF	183
Db	192	TEASREAEAAGFDGAVYVERAVINQHIEVQILGHTGEVWVHYERDCSILQRHORHVVEI	251
Db	184	HRAKSAEAKSFGNSEVYERYIDNKHIEVQIGEHDNTHFLFERDCSVORRHOKVVEI	243
QY	252	APAOHLDPEFRICADAVFCRFSYQGAGTVEFLV-DEKGNHVFIEINPRTOVENTV	309
QY	244	APSGVLSPTRLQRICDAAIOMENLYKVNAGTVEFLVSGNE--FFFENPVOVENTI	300
Db	310	TEEVTEVDLVKAQMLRAAGATL-KEGLTQDK-IKTHGALQCRITEDPPNGFRPTG	366
Db	301	TEMWVIGDITVTRTQOLVAAGDLFGEAEINMPQODITLTGVAIQRITTEDPPLNDPMDTG	360
QY	367	TITAVRSPGGAGVRLD-GAAQLGGETTAHEDSMLYKMTCTGSDFFETAVARAQRALEFTV	425
Db	361	TILAVRSGSGFGVRLDQAGQFQGRBISPYDLSVLYKLSTHAIISFQAEKMKRSIREMKI	420
QY	426	SGVATNIGFLRALLREDFEDTSKRIATGFLADPHLQOAPADDQGGRDITDYLADVTVNPK	485
Db	421	RGVKTNIPFLINVMNKKFTFSGYDTKFEETPELFDIOPSLDRGTKTLEYIGNATIN-	478
QY	486	HGVRKDKVAAPIDKLPNKLPLP-----RGSRDRKLQGPAFARD	527
Db	479	-----GFPNVEKPKPDYELASIPVSSSKTASFSGKPKQOLIDEVGPKGVAEW	525
Db	528	LREQDALAVTETTRDAHOSLALTRVRSFALKPKAAEAVAKLTPELLSVAAWGGTYDAM	587
Db	526	VKKPDDVLLTDTTERDAHOSLALTRVRSFALKPKAAEAVAKLTPELLSVAAWGGTYDAM	585
QY	588	RFLFDPWDRDLDELAEMPHQSLATRVTQKMDINIASTKADTVAKFUGKLSLEMWGATFAY	585
Db	586	NFLKENPWBRLERLURKATINPVLQMLRASNAVQYKNYFDMVHFKVQESAKAGIDVRI	645
QY	648	FDALNDVSMQRPDAIDAVLNTNTAVAEVAMAYSGDLSDLP-NEKLYTDYKLMAEIVKSG	706
Db	646	FDSLWNWDOMKVNANEAVQERG-KISEGTCITYGDLINPERSNTYLEYVUKLAKELERE	704
QY	707	ATHIAIKDMDGLLPAVVKLVTARREDPYHVFHHTDAGQOLATFAAAGADAVD	766
Db	705	FHIAIKDMDGLLPAVVKLVTARREDPYHVFHHTDAGQOLATFAAAGADAVD	764
QY	767	GASAPLGLSITQPSLSATVAAFAHTTRDGLSLEAVSLEPVGRLYLPFESGTGP	826
Db	765	TAVASMSGLTSQPSANSLYVLAGFPRHRTDLEGMSLSHWTYRYSIDESDKP	824
QY	827	TGRVYRHETPGQQLSNLRAQATAGLADRFELTEDNYAVNEMLGRPTKVTSSPKWVADL	886
Db	825	NTETYQHMPGQYSNLQSOQASLGLGERFEDYKMDYRVNFLEGDTKVTKVTSKVGMD	884
QY	887	ALHVGAGTDPAPFAADQKYDPSVAFRLRGLGNPGGPGPEPLRALLCERSEKAP	946
Db	885	ALXVNDLQDQSIVTGDYKLDPFESVVSFKGEIGQVNGFNDQQLAVLKGEE-A	940
QY	947	LTEVPEEAOHADDSE-----RWSLNRLIFPKTEEEFLRRFFGNTSAL	995
Db	941	LTARPGEELEPVEFEKRELLFEEQGQVPTEDDLSVLYPVYEQYIOTRQYGNLSS	1000

Query Match	43.0%	Score 2488; DB 22;	Length 1147;
Best Local Similarity	45.2%	Score 2488; DB 22;	Length 1147;
Matches 527; Conservative	192	Pred. No. 4.9e-174; Mismatches 384; Indels 62.	

Db 999 TFFNGIROTPELEVOIERRGT-LIRLDEIGEPIDGNDNRLFFNINGQRREVLVKDASK 1057
Qy 1059 SVTATAEKADSSNKHVAAPFAG-VVTVTVAEGDEVKA3DAVATEAMMKEATTIASVQG 1117
Db 1058 SAVQVKQKAPTNKEQIGAMMSGVILQVLVKRGDKVEKGOPPLITEAMMKTTEARFAG 1117
Qy 1118 KIDRVVVPAAATKVEGGDLIVV 1139
Db 1118 TVDHIVVEGEAISSGDLILEV 1139

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Job time : 68.5263 secs